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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

May 7, 2002, 12:08:25 ; Search time 54.19 Seconds (without alignments) 345.504 Million cell updates/sec

1 MDFQVQIFSFLLISASVILS............CQQWSSYPLTFGGGTKVEIK 128 US-09-772-103-8 655 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

473505 seqs, 146272329 residues Searched:

al number of hits satisfying chosen parameters:

 $\overline{\text{Minimum DB}}$ seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL_17:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_lnvertebrate:*
6: sp_mammal:* sp_vertebrate:*
sp_unclassified:* sp_mhc:*
sp_organelle:*
sp_phage:* sp_plant:* sp_rodent:* sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		מדחספחווו פחווו פסירניא
Ð	0901.77 0901.70 0901.81 0901.79 0901.79 0901.78 0911.84 0911.84 0911.85 0911.85 0911.83 0901.78 0991.83 0991.78 0991.78	
DB		
Query Match Length DB	108 108 108 108 109 109 109 101 109 101 101 103	
Query Match	66.6 65.7 66.2 66.2 66.2 66.2 66.2 66.3 66.3 66.3	
Score	436.5 428.5 411, 411, 411, 511, 511, 511, 511, 511	
Result No.	1 1 2 2 2 3 3 3 2 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	

Q9u180 homo sapien Q9n0w5 oryctolagus Q9nsd6 homo sapien Q9u182 homo sapien			C61243 mus musculu C61243 mus musculu C91b00 sphoeroides C99603 homo sapien C9udri homo sapien C9udri homo sapien	V9904 nome sapien Q99wi5 rattus norv Q9yhf9 ginglymosto O95775 homo sapien Q9hlu5 homo sapien P78324 homo sapien
114 4 Q9UL80 109 6 Q9NOW5 107 4 Q9NSD6 1107 4 Q9UL82 1107 4 Q9UL82	109 11 Q95M11 1109 1 Q95M113 130 4 Q9ND29 93 4 Q9UL76 1135 4 Q9H524 13 Q9H524	111111	123 11 Q61243 342 13 Q91800 122 4 Q99603 137 4 Q9UDR1 1168 4 Q9UQ56 122 4 Q99604	111444
297.5 45.4 1 294.5 45.0 1 241 36.8 1 206.5 36.1 2	20.00.00.00.00.00.00.00.00.00.00.00.00.0	21.7 21.1 20.8 20.8 20.2	19.9 19.9 19.1 19.0 19.5	121 18.5 51 117.5 17.9 11 117.5 17.9 11 117.5 17.9 3(
	•			4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

RESULT

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HSSP; P01679; ZFBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 62.7%
Best Local Similarity 70.9%
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                               Query Match 63.7%
Best Local Similarity 79.4%
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00406; 1Gv; 1.
NON_TER 1
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106
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Q9UL79
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SO FITTERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN *REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
HOMO Sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                     Clin. Immunol. Immunopathol. 87:184-192(1998).
-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 DIQMTQSPSSLSASVGDRVTITCSAISSIT-YMSWYQQKPGKAPKLLIYDTSNLASGVPS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                           Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.4%; Score 428.5; DB 4; Length 108; 78.5%; Pred. No. 5.7e-35; Live 9; Mismatches 13; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-98277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                           Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGSGTDFTLTISSLQPEDFATYCQQSYSTSWTFGEGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 AA.
                                                                                            108 AA.
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                                                                                                PRT;
                                                                                                                                                                                                                                                                                 MEDLINE-98277139; PubMed-9614934;
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EMBL; AF035033; AAD56269.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF035044; AAD56280.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P01607; IREI.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84; Conservative
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                                                                                                PRELIMINARY;
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SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
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Best Local Similarity
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Young D.C.;
                                                                                                                                                                                                                                                                                                                   Counq D.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                    fetus.";
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                                                                                                 09UL70
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Q9UL81

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SEQUENCE FROM N.A.
SONG X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan for chain
"Amplification, cloning and sequence analysis of the light chain
variable region gene of monoclonal anti-idiotypic antibody NP30 of
Schistosoma japonicum.";
Schistosoma japonicum.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 MTQSPSSLSASVGDRVTITCSATSSITYMSWYQQKPGKAPKLLIYDTSNLASGVPSRFSG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schistosoma japonicum (Blood fluke).
Eukaryota: Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
                                                                                                                                                                                                                                                                                                       2; Gaps
                                                                                                                                                                                                                                                                                                                                                   23 DIQWIQSPSSLSASVGDRVTITCSATSSIT-YMSWYQQKPGKAPKLLIYDTSNLASGVPS 81
                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 17, Last annotation update)
MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOCLOBULIN LIGHT CHAIN
VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                63.7%; Score 417; DB 4; Length 107; 79.4%; Pred. No. 7.7e-34; tive 8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 AA; 11478 MW; F20F544426BAE63E CRC64;
HSSP; P80362; 1WTL.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003596; Ig_V.
SPfam; PF00047; ig; 1.
SWART; SM00406; IGV; 1.
NON_TER 1 1 1
NON_TER 107 AN; 11501 MW; 070549FDE0754748 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF207620; AAF19434.1; -.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 2.
SMART; SM00406; IGv. 2.
SEQUENCE 298 AA; 31867 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
NON_TER
SEQUENCE
                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           fetus.";
                                                                                                                  Matches
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        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                 Clin. Immunol. Immunopathol. 87:184-192(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BALDC; TISSUE-SPLEEN;
Shinohara N., Demura T., Fukuda H.;
"Isolation of a novel type of vascular cell wall-specific monoclonal
antibody recognizing a cell polarity using a phage display subtraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                             23 DIQMTQSPSSLSASVGDRVTLTCSATSSI-TYMSWYQQKPGKAPKLLIYDTSNLASGVPS 81
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CN 8 SCFV.
CN 8.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                            Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                   Query Match 62.7%; Score 410.5; DB 4; Length 108; Best Local Similarity 75.7%; Pred. No. 3.4e-33; Matches 81; Conservative 9; Mismatches 16; Indels 1
                                                                                                                                      Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 3.4e-33;
9; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           82 RFSGSGSGTDYTLTISSLQPEDFATYYCQQWSSYPLTFGGGTKVEIK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BALB/C; TISSUE-SPLEEN;
Shinohara N., Demura T., Fukuda H.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                              108 AA; 11787 MW; DB5845F19724FB4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 AA
                                                                                                                          MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                  EMBL; AF035035; AAD56271.1; -. HSSP; P01607; 1REI. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB036341; BAA88633.1; -. HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                        108
                                                          Homo sapiens (Human).
                                                                                                               SEQUENCE FROM N.A.
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                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                      108
                                                                                                                                                                                                           DOMAIN
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SEQUENCE
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01-MAY-2000 (TrEWBLrel. 13, Last sequence update)
01-JUN-2001 (TrEWBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clin. Immunol. Immunopathol. 87:184-192(1998).
                                                                                                                                                           1; Gaps
                                                                                                                                      23 DIQMTQSPSSLSASVGDRVTITCSATSSI-TYMSWYQQKPGKAPKLLIYDTSNLASGVPS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 DIQMTQSPSSLSASVGDRVTITCSATSSI--TYMSWYQQKPGKAPKLLIYDTSNLASGVP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                           59.2%; Score 387.5; DB 11; Length 298; 67.3%; Pred. No. 2e-30; tive 18; Mismatches 16; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.1%; Score 387; DB 4; Length 109; 65.7%; Pred. No. 7.1e-31; tive 19; Mismatches 16; Indels
                                                                                                                                                                                                                   82 RFSGSGSGTDYTLTISSLQPEDFATYYCQQWSSYPLTFGGGTKVEIK 128
                                                                                                                                                                                                                                        81 SRFSGSGSGTDYTLTISSLQPEDFATYYCQQWSSYPLTFGGGTKVEIK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31867 MW; E0F96B8A17004317 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0DN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                    109 AA.
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                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed=9614934;
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EMBL, AF035036; AAD56272.1; -.
HSSP, P01789; IMMP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003396; Ig_V.
Pfam; PF00047; Ig; 1.
                                                                          Local Similarity 67.39
nes 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 65.78
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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RESULT 11
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                                                                                             Malkel S., Liao L., Cunningham M.W., Diamond B.; Malkel S., Liao L., Cunningham M.W., Diamond B.; Mcharacterization of cross-reactive monoclonal anti-myosin/anti-n-acety_slucosamine antibodies from mice with autoimmune myocarditis."; Submitted (NOV-1999) to the EMBL/GenBank/DDBU databases.
--- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                           1; Gaps
                                                                                                                                                                                                                                                                                                                                              23 DIQMTQSPSSLSASVGDRVTITCSATSSIT-YMSWYQQKPGKAPKLLIYDTSNLASGVPS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.9%; Score 379.5; DB 11; Length 214;
                                                                                                                                                                                                                                                                                                59.0%; Score 386.5; DB 11; Length 107; 71.0%; Pred. No. 7.7e-31;
                                                                                                                                                                                                                                                                                                                         19; Indels
                                                                                                                                                                                                                                                                                                                                                                                              214 AA; 23922 MW; 52BA205FDE995E2A CRC64;
                                                                                                                                                                                                                                                            107 AA; 11648 MW; ACF9B1253ACA1E5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NAY-2000 (TrEMBLrel. 13, Created)
01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 AA.
                                                                                                                                                                                                                                                                                                                           11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AFL52371; AAD40242.1; -. HSSP; P01789; IMCP.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 2.
SMART; SM00406; IGV: 1.
SMART; SM00410; IG_Like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                           EMBL; AF206022; AAF69320.1; -.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                              3est Local Similaria,
ustches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                 Mus musculus (Mouse).
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                                                                              SEQUENCE FROM N.A.
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                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                       107
                                                                                         STRAIN-BALB/C;
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NON_TER
SEQUENCE
                                                                                                                                                                    DOMAIN.
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Query Match

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Clin. Immunol. Immunopathol. 87:184-192(1998).
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01-MAY-2000 (TIEMBLEEL. 13, Last sequence update)
01-MAY-2001 (TIEMBLEEL. 17, Last annotation update)
01-JUN-2001 (TIEMBLEEL. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 DIQMTQSPSSLSASVGDRVTITCSATSSI-TYMSWYQQKPGKAPKLLIYDTSNLASGVPS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                   23 DIQMTQSPSSLSASVGDRVTITCSAISSI-TYMSWYQQKPGKAPKLLIYDTSNLASGVPS 81
                                                                                                                 1 DIQLTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MANTI-MYDOSIN IMMUNGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.3%; Score 375; DB 4; Length 109; 66.7%; Pred. No. 1.1e-29; Live 21; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 RESGSGSGTDYTLTISSLQPEDFATYYCQQWSSYPLTFGGGTKVEIK 128
                                                                                                                                                                                                    61 RFSGSGSGQDYSLTISSLEXEDMGIXYCLQYDEFPFTFGSGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11761 MW; FB1E43E7C7AFACCC CRC64;
Best Local Similarity 66.4%; Pred. No. 8.3e-30;
Matches 71; Conservative 15; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 AA.
                                                                                                                                                                                                                                                                                                                                                   109 AA.
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                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF035029; AAD56265.1; -. HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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Best Local Similarity 66.79
Matches 72; Conservative
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Q9JL76;
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Malkiel S., Liao L., Cunningham M.W., Diamond B.; "Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis."; submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEWBLrel. 13, Created)
01-MAY-2000 (TrEWBLrel. 13, Last sequence update)
01-JUN-2001 (TrEWBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               33 LSASVGDRVTITCSATSSITYMSWYQQKPGKAPKLLIYDTSNLASGVPSRFSGSGGTDY 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 DIQMTQSPSSLSASVGDRVTITCSATSSI-TYMSWYQQKPGKAPKLLIYDTSNLASGVPS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.6%; Score 364.5; DB 4; Length 108; 62.6%; Pred. No. 1.1e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                            13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;
                                                                                                                                                                                                                                                                                        97 AA; 10542 MW; C9EE1FFE1F49DA1C CRC64;
                                                                                                                                                                                                                                                                                                                                                         ch 56.9%; Score 372.5; DB 1. Similarity 73.2%; Pred. No. 1.7e-29; 71; Conservative 12; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 TLTISSLQPEDFATYYCQQWSS-YPLTFGGGTKVEIK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Mismatches
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                                                                                                                               EMBL; AF206030; AAF69328.1; -1 InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_V. Pfam; PF00047; Ig; 1. SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF035031; AAD56267.1; -. HSSP; P01607; 1REI.
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InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
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SEQUENCE
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Malkiel S., Liao L., Cunningham M.W., Diamond B.,;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
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-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TIWAASPGEKITITCSASSSISSNYLHWYQQRPGFSPKLLIYRTSNLASGVPTRFSGSGS 60
                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OUN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 55.2%; Score 361.5; DB 11; Length 101; Best Local Similarity 69.3%; Pred. No. 2.1e-28; Matches 70; Conservative. 17; Mismatches 11; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 GIDYILIISSLQPEDFATYYCQQWSSYP-LIFGGGTKVEIK 128
        101 AA.
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        PRT;
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MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL., AF206028, AAF69326.1; ... InterPro; IPR0033006; Ig_MHC. InterPro; IPR003596, Ig_V. Pfam; PF00047; ig; 1. ... SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                    STRAIN=A.CA;
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                           Q9JL78;
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Q9JL78
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:5947).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 52.1%; Score 341; DB 11; Length 238; Best Local Similarity 57.4%; Pred. No. 5.8e-26; Matches 66; Conservative 15; Mismatches 28; Indels
                                                                                      Query Match 55.1%; Score 361; DB 4; Length 109; Best Local Similarity 62.0%; Pred. No. 2.6e-28; Matches 67; Conservative 20; Mismatches 19; Indels
                                                                                                                                                                                                       Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002035; AAH02035.1; -.
SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;
SWART; SM00406; IGV; 1.

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SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;
                                                                                                                                                                                                                                                                                                               238 AA.
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                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=MAMMARY TUMOR;
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